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1. *Phragmites australis* (Cav.) Trin. ex Steud.

Figure 1B

961	CTTCCCTTGGAGGCTACATCTGGGCTATTATCTCAAGTTTAACTTTCTGAGCAGGCT	961
1001	R P P E E Y T P E Y Y L K F N F L E A	1001
961	TTAGACAAAGTGTCTGAGTGGGGCTTCCACATGCTGGGGCTGTAGCTTATCGGGACCTGG	1020
1001	F D K L S E S G F H M V A C S S T G T C	1020
1021	GGCTTTGGGAGCAGGACCGAGAGCGAGGACAGATCTGGACCGAGCTACACCGAGTAC	1080
1001	A F A S S T D Q S E D K I W T S Y T E Y	1080
1081	GTCTTCTGGAGGGAGTGGAGTGGGACAGCCCTCTGGCCACTCCAGCGGCGGAGTCTCTCT	1140
1001	V F C R E	1140
1141	CTGCCCCGAGAGATGATTACAGAGCCTCTTGTCCACCTTTGTCCCCCTGGCTGCTGGCCCTC	1200
1201	CCATTCTCCCCCTCCAGTAGTAGCTGGGTGAGACCTGTCCGCCACCTTCCCTCCACTAC	1260
1261	AGAACCTGCAGCGCGCAAATCCTCTGGGCTGCTTCTGTCTTCTTTGGACCTCTCGAACCGAG	1320
1321	AGAACCCAGAGGAACCCCCACCCCCACCCCCACCTACCACTCCATGCTTTCTCTACTCCCT	1380
1381	GGCTCAAAACCGCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGAGTGTGGC	1440
1441	CACAGACCGGGGGGATGATTGAATTGTTTCAGAACCTGATTGGACCGGTGCCAATGTGCGGA	1500
1501	AGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAGATCAGGAT	1560
1561	TGGTTCCACTGTCTGGGGTTAGTGTTTTTACAAGGTCATTACACAGTCTTTTGGACCTCTT	1620
1621	TTGAAGGTAGAGTTTTAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAGGACCCCAT	1680
1681	GGAGGCAGTCCCTCAAACCCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGG	1740
1741	AGTSTGGCCACAGACCGSSGGATGATTGAATTGTTTCAGAACCTGATTGGACCGTGTCCAA	1800
1801	TGTGGGGAAGATTTCTTGAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAG	1860
1861	ATCAGGATTGGTTCAGTCTTGGGGTTAGTGTCTTACAAGGTCATTACACAGTCTTTTT	1920
1921	GAGTCTTTTTGAAGGTAGATTTTGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTGAGCGTGAATTAG	1980

Figure 1C

1941 GAATGATGAGGCAATTCAGTAACTAACTAATAAAATTTTGAAGAAATTACATATAGAA 1940

2041 AAAAAAAAAA 2051

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Figure 2B

		331	351
K+betaM6	(196)	CTATATAGAGT--DQEDKINTSYTEYWFDEE	
KCNMB1	(192)		
K+Hnov27	(222)	GSFVDSQFLRYTLRRELRRTPRUPVIRIKLEL	
K+Hnov28	(204)	TIRNIEFHMMHFAFANETLEHNTWFRLAKHDT	
KIAA1317	(259)	SEVTAFFIN---QYDDKINSSYTEYWFYEEFQWSPQHLLQYNNKH	
CG10465	(267)	YGNASSTEIN.YTSDEEEERTSLARLRNNHFLNPL	
CG10830	(196)	GSSTAGSAAEPKPGVDTTEENKNNHYNEFWFID	
K+channel_tetra	(141)		
		351	400
K+betaM6	(326)		
KCNMB1	(192)		
K+Hnov27	(257)		
K+Hnov28	(238)		
KIAA1317	(304)	GDKESESSTGNDLSTSSSDSQSEASSPQETNIGSPVTRQTNIQLDRPI	
CG10465	(302)		
CG10830	(229)		
K+channel_tetra	(141)		
		401	450
K+betaM6	(326)		
KCNMB1	(192)		
K+Hnov27	(257)		
K+Hnov28	(238)		
KIAA1317	(354)	KKGPVQLIQQSEMRKSDLLRTLTSGRRESNMSSKKKAVKEKLSIEEELE	
CG10465	(302)		
CG10830	(229)		
K+channel_tetra	(141)		
		451	482
K+betaM6	(326)		
KCNMB1	(192)		
K+Hnov27	(257)		
K+Hnov28	(238)		
KIAA1317	(404)	KCIQDFLKIFIPDRFPERKHPWQSELLRKYHL	
CG10465	(302)		
CG10830	(229)		
K+channel_tetra	(141)		

Figure 3

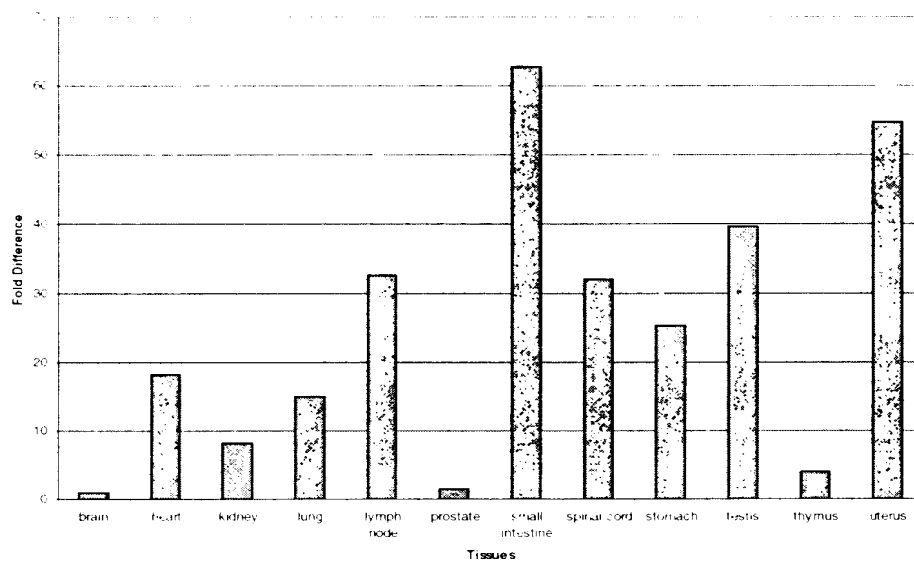


Figure 4.

<u>Protein</u>	<u>Genbank / SWISS- PROT Accession No.</u>	<u>Identities</u>	<u>Similarities</u>
human Maxi-K potassium channel beta subunit, KCNMB1 protein	gil4758625	0.0%	37.5%
human potassium channel K+Hnov27 protein	gilY34125	30.21%	39.15%
human potassium channel K+Hnov28 protein	gilY34129	30.04%	38.63%
Caenorhabditis elegans K+ channel tetramerisation domain containing protein	gil3880445	31.11%	39.26%
Drosophila CG10465 protein	gil17946205	23.9%	33.0%
Drosophila CG10830 protein	gil7300672	50.89%	62.5%
human KIAA1317 protein	gil7243015	60.42%	69.97%

